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SEQUENCE LISTING

<110> HAMILTON, STEPHEN <120> ENDOMANNOSIDASES IN THE MODIFICATION OF GLYCOPROTEINS IN EUKARYOTES <130> GFI/109 CIP <140> 10/695,243 <141> 2003-10-27 <150> 10/371,877 <151> 2003-02-20 <160> 29 <170> PatentIn Ver. 3.2 <210> 1 <211> 1389 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(1386) <400> 1 atg gca aag ttt cgg aga agg act tgc atc att ttg gca ctt ttt att Met Ala Lys Phe Arg Arg Thr Cys Ile Ile Leu Ala Leu Phe Ile cta ttt att ttc tct ctg atg atg ggt tta aaa atg ctg aga cca aat 96 Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn aca gct act ttt gga gct cct ttt gga ctt gac ctt ctt cca gaa ctt 144 Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu cat caa cga act att cat ttg ggg aaa aat ttt gat ttc caa aag agt 192 His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser gac aga atc aac agt gaa aca aat acc aag aat tta aaa agt gtt gaa 240 Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu 65 75 atc act atg aaa cct tcc aaa gcc tct gaa ctt aac ttg gat gaa cta Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu 85 90

cca Pro	cct Pro	ctg Leu	aac Asn 100	Asn	tat Tyr	cta Leu	cat His	gta Val 105	Phe	tat Tyr	tac Tyr	agt Ser	tgg Trp	Туг	gga Gly	336
aat Asn	cca Pro	caa Gln 115	Phe	gat Asp	ggt Gly	aaa Lys	tat Tyr 120	Ile	cat His	tgg Trp	aat Asr	cat His 125	Pro	gtg Val	tta Leu	384
gag Glu	cat His 130	Trp	gac Asp	cct Pro	aga Arg	ata Ile 135	Ala	aag Lys	aat Asn	tat Tyr	Pro	Gln	ggg Gly	aga Arg	cac His	432
aac Asn 145	Pro	cca Pro	gat Asp	gac Asp	att Ile 150	ggc Gly	tcc Ser	agc Ser	ttt Phe	tat Tyr 155	Pro	gaa Glu	ttg Leu	gga Gly	agt Ser 160	480
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gta Val	aat Asn	gat Asp 195	gaa Glu	aat Asn	gga Gly	gaa Glu	cct Pro 200	act Thr	gat Asp	aac Asn	ttg Leu	gta Val 205	ccc Pro	act Thr	att Ile	624
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cca Pro 225	tat Tyr	agc Ser	aat Asn	cga Arg	gat Asp 230	gat Asp	caa Gln	aac Asn	atg Met	tac Tyr 235	aaa Lys	aat Asn	gtc Val	aag Lys	tat Tyr 240	720
att Ile	ata Ile	gac Asp	aaa Lys	tat Tyr 245	gga Gly	aat Asn	cat His	ccg Pro	gcc Ala 250	ttt Phe	tac Tyr	agg Arg	tac Tyr	aag Lys 255	acg Thr	768
aag Lys	act Thr	ggc Gly	aat Asn 260	gct Ala	ctt Leu	cct Pro	atg Met	ttt Phe 265	tat Tyr	gtc Val	tat Tyr	gat Asp	tcc Ser 270	tat Tyr	att Ile	816
acc Thr	aag Lys	cct Pro 275	gaa Glu	aaa Lys	tgg Trp	gcc Ala	aat Asn 280	ctg Leu	tta Leu	acc Thr	acc Thr	tca Ser 285	G1Y 999	tct Ser	cgg Arg	864
agt Ser	att Ile 290	cgc Arg	aat Asn	tct Ser	cct Pro	tat Tyr 295	gat Asp	gga Gly	ctg Leu	ttt Phe	att Ile 300	gcc Ala	ctt Leu	ctg Leu	gta Val	912

	gaa Glu															960
	aca Thr															1008
aat Asn	tgg Trp	gct Ala	agc Ser 340	cta Leu	aaa Lys	tta Leu	att Ile	tgt Cys 345	gat Asp	aaa Lys	tac Tyr	aac Asn	tta Leu 350	ata Ile	ttt Phe	1056
	cca Pro															1104
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ggt Gly 385	ctg Leu	agt Ser	gcc Ala	gca Ala	ctt Leu 390	cag Gln	aca Thr	cgc Arg	ccc Pro	agc Ser 395	tta Leu	att Ile	tct Ser	atc Ile	acc Thr 400	1200
tct Ser	ttt Phe	aat Asn	gag Glu	tgg Trp 405	cat His	gaa Glu	gga Gly	act Thr	cag Gln 410	att Ile	gaa Glu	aaa Lys	gct Ala	gtt Val 415	ccc Pro	1248
aaa Lys	aga Arg	acc Thr	agt Ser 420	aat Asn	aca Thr	gtg Val	tac Tyr	cta Leu 425	gat Asp	tac Tyr	cgt Arg	cct Pro	cat His 430	aaa Lys	cca Pro	1296
ggt Gly	ctt Leu	tac Tyr 435	cta Leu	gaa Glu	ctg Leu	act Thr	cgc Arg 440	aag Lys	tgg Trp	tct Ser	gaa Glu	aaa Lys 445	tac Tyr	agt Ser	aag Lys	1344
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<210> 2

<211> 462 <212> PRT

<213> Homo sapiens

<400> 2

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Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn 20 25 30

- Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu 35 40 45
- His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser 50 55 60
- Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu 65 70 75 80
- Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu 85 90 95
- Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly
 100 105 110
- Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu 115 120 125
- Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His 130 135 140
- Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser 145 150 155 160
- Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met
 165 170 175
- Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp 180 185 190
- Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu Val Pro Thr Ile 195 200 205
- Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr Phe His Ile Glu 210 215 220
- Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys Asn Val Lys Tyr 225 230 235 240
- Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr Arg Tyr Lys Thr 245 250 255
- Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr Asp Ser Tyr Ile 260 265 270
- Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr Ser Gly Ser Arg
 275 280 285
- Ser Ile Arg Asn Ser Pro Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val 290 295 300
- Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile 305 310 315 320

Tyr	Thr	Tyr	Phe	Ala 325		Asn	Gly	, Phe	330		Gly	/ Ser	Ser	His 335	s Gln	
Asn	Trp	Ala	Ser 340	Leu	Lys	Leu	Il∈	Cys 345		Lys	туг	Asn	Let 350		Phe	
Ile	Pro	Ser 355	Val	Gly	Pro	Gly	Tyr 360		e Asp	Thr	Ser	: Ile 365		J Pro	Trp	
Asn	Thr 370	Gln	Asn	Thr	Arg	Asn 375	Arg	Ile	Asn	Gly	7 Lys 380		Tyr	Glu	ılle	
Gly 385	Leu	Ser	Ala	Ala	Leu 390	Gln	Thr	Arg	Pro	Ser 395		Ile	Ser	Ile	Thr 400	
Ser	Phe	Asn	Glu	Trp 405	His	Glu	Gly	Thr	Gln 410		Glu	Lys	Ala	Val 415	Pro	
Lys	Arg	Thr	Ser 420	Asn	Thr	Val	Tyr	Leu 425		Tyr	Arg	Pro	His 430	_	Pro	
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cta i Leu i	ttt Phe	att Ile	ttt Phe 20	tct Ser	ctg Leu	atg Met	atg Met	ggc Gly 25	tta Leu	aag Lys	atg Met	ctg Leu	tgg Trp 30	cca Pro	aac Asn	96
gca g Ala A	gca Ala	tcc Ser 1 35	ttt (Phe (gga Gly	cct Pro	cct Pro	ttt Phe 40	gga Gly	ctt Leu	gac Asp	ctc Leu	ctt Leu 45	cca Pro	gaa Glu	ctt Leu	14

cat cca cta aat gcg cat tcg gga aac aaa gct gac ttc caa agg agt His Pro Leu Asn Ala His Ser Gly Asn Lys Ala Asp Phe Gln Arg Ser

	Arg										Let				ggc Gly 80	240
atg Met	g act Thr	gtg Val	ctg Leu	cca Pro 85	Ala	aaa Lys	gcc Ala	tct Ser	gag Glu 90	Val	aac Asn	ctg Leu	gaa Glu	gaa Glu 95	cta Leu	288
cct Pro	cct Pro	ctg Leu	aat Asn 100	Tyr	ttt Phe	tta Leu	cat His	gca Ala 105	Phe	tat Tyr	tac Tyr	agt Ser	tgg Trp 110	Tyr	gga Gly	336
aat Asr	cca Pro	cag Gln 115	ttt Phe	gat Asp	ggt Gly	aaa Lys	tat Tyr 120	Ile	cac His	tgg Trp	aat Asn	cat His 125	ccg Pro	gtc Val	ctg Leu	384
gaa Glu	cac His 130	\mathtt{Trp}	gac Asp	cct Pro	cgg Arg	ata Ile 135	gcc Ala	aag Lys	aac Asn	tat Tyr	cca Pro 140	Gln	gga Gly	caa Gln	cat His	432
agt Ser 145	cct Pro	cca Pro	gac Asp	gac Asp	att Ile 150	ggc	tcc Ser	agt Ser	ttt Phe	tat Tyr 155	cct Pro	gag Glu	tta Leu	gga Gly	agt Ser 160	480
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cgc Arg	tca Ser	gcc Ala	tca Ser 180	att Ile	gga Gly	gtt Val	ctg Leu	gcc Ala 185	ctg Leu	tct Ser	tgg Trp	tac Tyr	cca Pro 190	cct Pro	gat Asp	576
tca Ser	agg Arg	gat Asp 195	gac Asp	aat Asn	ggc Gly	gaa Glu	gct Ala 200	act Thr	gat Asp	cac His	ttg Leu	gtg Val 205	cca Pro	acc Thr	att Ile	624
ttg Leu	gat Asp 210	aaa Lys	gct Ala	cat His	aaa Lys	tat Tyr 215	aat Asn	ctg Leu	aag Lys	gtc Val	act Thr 220	ttt Phe	cac His	ata Ile	gag Glu	672
cca Pro 225	tat Tyr	agc Ser	aat Asn	cga Arg	gat Asp 230	gat Asp	caa Gln	aac Asn	atg Met	cat His 235	caa Gln	aat Asn	atc Ile	aag Lys	tat Tyr 240	720
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agg Arg	act Thr	gly aaa	cat His 260	tct Ser	ctg Leu	ccc Pro	atg Met	ttt Phe 265	tat Tyr	gtc Val	tat Tyr	gat Asp	tct Ser 270	tac Tyr	atc Ile	816

aca Thr	aag Lys	cct Pro 275	Thr	ata Ile	tgg Trp	gcc Ala	aat Asn 280	Leu	tta Leu	aca Thr	ccc Pro	s tcc Ser 285	Gly	tct Ser	cag Gln	864
agt Ser	gtt Val 290	cgc Arg	agt Ser	tct Ser	ctt Leu	tat Tyr 295	Asp	gga Gly	ttg Leu	ttt Phe	att Ile 300	Ala	ctt Leu	cta .Leu	gta Val	912
gaa Glu 305	Glu	aag Lys	cat His	aaa Lys	aat Asn 310	Asp	att Ile	ctt Leu	cag Gln	agt Ser 315	ggt Gly	ttt Phe	gat Asp	ggt Gly	att Ile 320	960
tac Tyr	aca Thr	tat Tyr	ttt Phe	gcc Ala 325	aca Thr	aat Asn	ggc	ttt Phe	aca Thr 330	Tyr	ggc	tca Ser	tct Ser	cat His 335	cag Gln	1008
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Asn	370	Gln	Asn	Thr	Arg	Asn 375	Arg	Val	Asn	Gly	aag Lys 380	Tyr	Tyr	Glu	Val	1152
385	Leu	ser	Ala	Ala	190	Gln	Thr	His	Pro	Ser 395	tta Leu	Ile	Ser	Ile	Thr 400	1200
ser	Pne	ASN	GIU	1rp 405	HIS	Glu	Gly	Thr	Gln 410	Ile	gaa Glu	Lys	Ala	Val 415	Pro	1248
2,5	Arg	1111	420	ASII	inr	11e	Tyr	Leu 425	Asp	Tyr	cgg Arg	Pro	His 430	Lys	Pro	1296
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gaa Glu	aga Arg 450	atg Met	acg Thr	tat Tyr	Ala	ttg Leu 455	gat Asp	caa Gln	cag Gln	cag Gln	cct Pro 460	gct Ala	tca Ser	taa		1389

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<211> 462 <212> PRT <213> Mus musculus

<400> 4

Met Ala Lys Phe Arg Arg Thr Cys Ile Leu Leu Ser Leu Phe Ile 1 5 10 15

Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Trp Pro Asn 20 25 30

Ala Ala Ser Phe Gly Pro Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu 35 40 45

His Pro Leu Asn Ala His Ser Gly Asn Lys Ala Asp Phe Gln Arg Ser 50 55 60

Asp Arg Ile Asn Met Glu Thr Asn Thr Lys Ala Leu Lys Gly Ala Gly 65 70 75 80

Met Thr Val Leu Pro Ala Lys Ala Ser Glu Val Asn Leu Glu Glu Leu 85 90 95

Pro Pro Leu Asn Tyr Phe Leu His Ala Phe Tyr Tyr Ser Trp Tyr Gly
100 105 110

Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu 115 120 125

Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Gln His 130 135 140

Ser Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser 145 150 155 160

Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Lys Gln Met 165 170 175

Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp 180 185 190

Ser Arg Asp Asp Asn Gly Glu Ala Thr Asp His Leu Val Pro Thr Ile 195 200 205

Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr Phe His Ile Glu 210 215 220

Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met His Gln Asn Ile Lys Tyr 225 230 235 240

Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr Arg Tyr Lys Thr 245 250 255

Arg Thr Gly His Ser Leu Pro Met Phe Tyr Val Tyr Asp Ser Tyr Ile 260 265 270

Thr Lys Pro Thr Ile Trp Ala Asn Leu Leu Thr Pro Ser Gly Ser Gln 275 280 285

Ser Val Arg Ser Ser Leu Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val 290 295 300

Glu Glu Lys His Lys Asn Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile 305 310 315 320

Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln 325 330 335

Asn Trp Asn Asn Leu Lys Ser Phe Cys Glu Lys Asn Asn Leu Met Phe 340 345 350

Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser Ile Arg Pro Trp 355 360 365

Asn Thr Gln Asn Thr Arg Asn Arg Val Asn Gly Lys Tyr Tyr Glu Val 370 375 380

Gly Leu Ser Ala Ala Leu Gln Thr His Pro Ser Leu Ile Ser Ile Thr 385 390 395 400

Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro 405 410 415

Lys Arg Thr Ala Asn Thr Ile Tyr Leu Asp Tyr Arg Pro His Lys Pro 420 425 430

Ser Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu Lys Phe Ser Lys 435 440 445

Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Gln Pro Ala Ser 450 455 460

<210> 5

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 5

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<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

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<210> 7
<211> 59
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<213> Artificial Sequence
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<210> 8
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
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                                                                   40
<210> 9
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                                                                    44
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<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
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<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 15
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<210> 16
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      primer
<400> 16
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<400> 17
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<400> 19
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<210> 23

<211> 290

<212> PRT

<213> Rattus norvegicus

<400> 23

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Tyr Pro Pro Asp Ala Ser Asp Glu Asn Gly Glu Ala Thr Asp Tyr Leu 20 25 30

Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr 35 40 45

Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met His Gln 50 55 60

Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr 65 70 75 80

Arg Tyr Lys Thr Arg Met Gly His Ser Leu Pro Met Phe Tyr Ile Tyr 85 90 95

Asp Ser Tyr Ile Thr Lys Pro Lys Thr Trp Ala Asn Leu Leu Thr Pro 100 105 110

Ser Gly Ser Gln Ser Val Arg Gly Ser Pro Tyr Asp Gly Leu Phe Ile 115 120 125

Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly
130 135 140

Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly 145 150 155 160

Ser Ser His Gln Asn Trp Asn Lys Leu Lys Ser Phe Cys Glu Lys Asn 165 170 175

Asn Met Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser

Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys
195 200 205

Tyr Tyr Glu Val Gly Leu Ser Ala Ala Leu Gln Thr Gln Pro Ser Leu 210 225 220

Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu 225 230 235 240

Lys Ala Val Pro Lys Arg Thr Ala Asn Thr Val Tyr Leu Asp Tyr Arg 245 250 255

Pro His Lys Pro Ser Leu Tyr Leu Glu Ile Thr Arg Lys Trp Ser Glu 260 265 270

Lys Tyr Ser Lys Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Leu Pro 275 280 285

Ala Ser 290

<210> 24

<211> 290

<212> PRT

<213> Homo sapiens

<400> 24

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Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr 35 40 45

Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys
50 55 60

Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr 65 70 75 80

Arg Tyr Lys Thr Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr 85 90 95

Asp Ser Tyr Ile Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr 100 105 110

Ser Gly Ser Arg Ser Ile Arg Asn Ser Pro Tyr Asp Gly Leu Phe Ile 115 120 125

Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly 130 135 140

Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly
145 150 155 160

Ser Ser His Gln Asn Trp Ala Ser Leu Lys Leu Phe Cys Asp Lys Tyr 165 170 175

Asn Leu Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser 180 185 190

Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys
195 200 205

Tyr Tyr Glu Ile Gly Leu Ser Ala Ala Leu Gln Thr Arg Pro Ser Leu 210 215 220

Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu 225 230 235 240

Lys Ala Val Pro Lys Arg Thr Ser Asn Thr Val Tyr Leu Asp Tyr Arg 245 250 255

Pro His Lys Pro Gly Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu 260 265 270

Lys Tyr Ser Lys Glu Arg Ala Thr Tyr Ala Leu Asp Arg Gln Leu Pro 275 280 285

Val Ser 290

<210> 25

<211> 195

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Lys Phe Arg Arg Arg Thr Cys Ile Ile Leu Ala Leu Phe Ile 1 5 10 15

Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn 20 25 30

Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu 35 40 45

His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser

Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu 65 70 75 80

Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu 85 90 95 Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly
100 105 110

Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu 115 120 125

Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His 130 135 140

Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser 145 150 155 160

Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met 165 170 175

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Val Asn Glu 195

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Asp Phe Gln Arg Ser Asp Arg Ile Asp Met Glu Thr Asn Thr Lys Asp 50 55 60

Leu Lys Gly Ala Gly Val Thr Val His Pro Pro Arg Ala Ser Glu Val 65 70 75 80

Asn Leu Glu Glu Leu Pro Pro Leu Asn Tyr Phe Val His Ala Phe Tyr 85 90 95

Tyr Ser Trp Tyr Gly Asn Pro Gln Phe Asp Gly Lys Tyr Val His Trp
100 105 110

Asn His Pro Val Leu Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr 115 120 125

Pro Gln Gly Arg His Ser Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr 130 135 140

Pro Glu Leu Gly Ser Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Lys Gln Met Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser 170 Trp Tyr Pro Pro Asp Ala Ser Asp Glu Asn Gly Glu Ala Thr Asp Tyr Leu Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val 200 Thr Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met His 210 215 220 Gln Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe 230 Tyr Arg Tyr Lys Thr Arg Met Gly His Ser Leu Pro Met Phe Tyr Ile 245 Tyr Asp Ser Tyr Ile Thr Lys Pro Lys Thr Trp Ala Asn Leu Leu Thr Pro Ser Gly Ser Gln Ser Val Arg Gly Ser Pro Tyr Asp Gly Leu Phe 275 Ile Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr 305 315 Gly Ser Ser His Gln Asn Trp Asn Lys Leu Lys Ser Phe Cys Glu Lys 330 Asn Asn Met Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr 345 Ser Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly 360 Lys Tyr Tyr Glu Val Gly Leu Ser Ala Ala Leu Gln Thr Gln Pro Ser 375 380 Leu Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile 395 400 Glu Lys Ala Val Pro Lys Arg Thr Ala Asn Thr Val Tyr Leu Asp Tyr

410

Arg Pro His Lys Pro Ser Leu Tyr Leu Glu Ile Thr Arg Lys Trp Ser

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